



GH74\_Ace — DYAE LNPSIIVRAGSFDPSSQPNDRHVAFSTDG GKNWFQ GSEPGGVTTGGTVAASADGSR  
AvIII\_Aac — DYAGNKPSNIVRSGASDDYP — TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT

GH74\_Ace FWWAPGDPQGPVVYAVGFGNSWAASQGVPANAIQRSDRVNPKTFYALSNGTFYRSTDGGV  
AviIII\_Aac VLLMSSTSGALVSKSQG-TLTAVSSLP SGAVIASDKSDNTVFYGGSGAGIYVSKNTAT

GH74\_Ace — TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGCSSWSAI TGVSSAVNV  
AviIII\_Aac — SFTKTVS LGSSTTVNAIR AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF

GH74\_Ace — GFGKSAPGSSYPAVFWGTIGGVTGAYRSDDCGTTWVLINDDQHQYGNWQQAITGDHAN  
AvIII\_Aac — GFGKASSTGSYVAIYGFETIDGAAGLFKSEDACTNWWQVISDASHGFGSGSANVA/NGDLQT

GH74\_Ace—LRRVYIGTNGRGIVYGDIGGAPSG  
AviIII\_Aac—YGRVFRGHERPGHLLRQSQREPAG

2. (Previously Amended) The composition of claim 1 wherein the AvIII peptide is further defined as comprising a linker and a signal sequence.
3. (Previously Cancelled)
4. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AvIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AvIII peptide is further defined as comprising a length of about 90 amino acids.
6. (Previously Amended) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.
7. (Previously Amended) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Previously Amended) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.
9. (Previously Amended) The composition of claim 1 wherein said AvIII protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.
10. (Previously Amended) The composition of claim 1, wherein the catalytic domain of GH74\_Ace has at least 90% sequence identity with SEQ ID NO: 3.
11. (Previously Amended) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.
12. (Previously Amended) An isolated AvIII peptide having a polypeptide sequence of SEQ ID NO: 1.
13. (Cancelled)
14. (Previously Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the AvIII polypeptide of claim 1.
15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[.]
- 16-27 (Cancelled)
28. (Previously Amended) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:
  - a) a polypeptide sequence of SEQ ID NO: 3;
  - b) a polypeptide sequence of SEQ ID NO: 4;

- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Previously Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Amended) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII\_Aac):

GH74\_Ace    ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAAANGRWIPLLDWVG  
 AvIII\_Aac    AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG  
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 ...\* \*\*

GH74\_Ace WNNWGYNGVVSIAADPINTNKVWAAVGMYSNSWDPNDGAILRSSDQGATWQITPLPFKLG  
AvIII\_Aac NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDWTETKLPFKVG  
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GH74\_Ace      GNMPGRGMGERLAVDPNNDNIFYGAPSGKGLWRSTDGATWSQMTNFPDVGTYIANPTD  
AviIII\_Aac    GNMPGRGMGERLAVDPNKNISILYFGARSGHGLWKSTDYGATWSNVTSTFTWTGTYFQDSSS  
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GH74\_Ace TTGYQSDIQGVVWVAFDKSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T  
AvIII\_Aac T--YTSDPVGIAVWTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY  
\* \* \* \* \*, \*\*,\*, \* \* \*, \* \* \*, \* \* \*, \* \* \*, \* \* \*, \* \* \*

GH74\_Ace      GFIPHKGVFDPVNHVLIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF  
AviIII\_Aac    GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNTSGVWTDISP---TSLASTYY  
                 \*\*,\*\*\*\*\*,\*.,\*\*.,\*.\* \*\*\*\*\*,\*.\*.,\*\*\*\*\* \*\*\*,\*.,

GH74\_Ace GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSRLRYVLDIS  
AviIII\_Aac GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDGATWSPIWEWNGYPSINYYYYSYDIS  
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GH74\_Ace AEPWLTFGVQPNPPVPSPKLGWMDEAMADPFNSDRMLYGTGATLYATNDLTKWDSSGGQI  
AvIII\_Aac NAPWIQDSTTDQFP--VRVGWMVEALADPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV

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GH74\_Ace      HIAPMVGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV  
AvIII\_Aac    TVKSLAVGIEEMAVLGITPPGGPALLSAVGDDGGFYHSDLAAPNQAYHTPTYGTNGI

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GH74\_Ace   DYAELNPSIIVRAGSFDPSQPNDRHVAFSTDGKNWFQGGSEPGGVTTGGTVAASADGSR  
AvIII\_Aac   DYAGNKPSNIVRSGASDDYP-----TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT  
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GH74\_Ace FVWAPGDPGPVVYAVGFNGSWAASQGVPAQAIRSDRVNPKTFYALSNGTFYRSTDGGV  
AvIII\_Aac VLLMSSTSGALVSKSQG---TLTAVSSLPAGAVIASDKSNTVFYGGSGAGIYVSKNTAT

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GH74\_Ace TFQPPAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV  
AvIII\_Aac SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF  
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GH74\_Ace      GFGKSAPGSSYPAVFVVGTTGGVTGAYRSDDCGTTWVLINDDQHGYGN-WGQAITGDHAN  
 AvIII\_Aac    GFGKASSTGSYVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVGDLQT  
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GH74\_Ace LRRVYIGTNGRGIVYGDIGGAPSG  
Avilll\_Aac YGRVFRGHERPGHLLRQSQREPAG  
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48. (New) The composition of claim 47 wherein said AvIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (New) A composition comprising a substantially purified AvIII peptide having at least 99% identity to SEQ ID NO. 1, said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (New) The composition of claim 49 wherein said catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII Aac):

GH74\_Ace ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAAANGRWIPLLDWVG  
AviIII\_Aac AASQAYTWKNVVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG  
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GH74\_Ace WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPN DGAILRSSDQGATWQITPLPFKLG  
Avillt\_Aac NDTWHDWGIDALATDPVDTRVYVAVGMYTNEWDPNVGSILRSTDQGDWTETKLPFKV G

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GH74\_Ace      GNMPGRGMGERLAVDPNNDNIFYLGAPSGKGLWRSTDGATWSQMTNFPDVGTYIANPTD  
 Avilli\_Aac    GNMPGRGMGERLAVDPNKNLSIFYLGARSGHGLWKSTDYATWSNVTSFTWTGTYFQDSSS  
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GH74\_Ace    TTGYQSDIQGVVWVAFDKSSSSSLGQASKTIFVGVADPNPNPVFWSRDGGATWQAVPGAP-T  
 Avill1\_Aac   T-YTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY  
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GH74\_Ace      GFIPHKGVDFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISVPSTDTANDYF  
 Avilll\_Aac    GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNI TSGVWTDISP---TSLASTYY  
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GH74\_Ace GYSGLTIDRQHPTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSRLRYVLDIS  
Avilll\_Aac GYGGLSVDLQVPGLTMVAALNCWWPDELIFRSTDGATWSPIWEWNGYPSINYYYYSYDIS

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GH74\_Ace AEPWLTFGVQPNPPVSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI  
AvIII\_Aac NAPWIQDSTTDQFP--VRVGWMVEALADPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV  
\*\* . . . . . \*\*\*\* \*\* . . . . . \*\*\*\* \*\* . . . . . \*\*\*\* \*\* . . . . .

GH74\_Ace      HIAPMVGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV  
AviIII\_Aac    TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLAAPNQAYHTPTYGTNGI

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GH74\_Ace      DYAE LNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR  
Avilll\_Aac    DYAGNKPSNIVRSGASDDYP-----TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT

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